



Conseiller.ST25
SUBSTITUTE SEQUENCE LISTING

<110> Conseiller, Emmanuel
Debussche, Laurent
Gallagher, William

<120> Polypeptide (MBP1) Capable of Interacting with Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 09/829,936

<141> 2001-04-11

<150> FR9812754

<151> 1998-10-12

<160> 35

<170> PatentIn version 3.3

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5'-1(p53)

<400> 1

agatctgtat ggaggagccg cag

23

<210> 2

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' -393 (p53)

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<400> 2
agatctcatc agtctgagtc aggcccttc 29

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide H175 3'

<400> 3
ggggcagtgc ctcac 15

<210> 4

<211> 15

<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide w248 3'

<400> 4
gggcctccag ttcac 15

<210> 5

<211> 15

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide H273 3'

<400> 5
acaaacatgc acctc 15

<210> 6

<211> 15

<212> DNA

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<213> Artificial Sequence

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<223> oligonucleotide G281 3'

<400> 6
gccccggcct ctccc

15

<210> 7

<211> 23

<212> DNA

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<223> Oligonucleotide 5'-73

<400> 7
agatctgtgt ggcccttgca cca

23

<210> 8

<211> 1021

<212> DNA

<213> Artificial Sequence

<220>
<223> Murine MBP1 C-term fragment

<220>
<221> CDS
<222> (1)..(885)

<400> 8
tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg gac
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

48

ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

96

ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

144

aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

192

tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys

240

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65	70	75	80	
aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile 85 90 95				288
gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn 100 105 110				336
gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu 115 120 125				384
gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His 130 135 140				432
caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac cgc Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg 145 150 155 160				480
tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp 165 170 175				528
aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag cct Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro 180 185 190				576
tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val 195 200 205				624
cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt gcc Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala 210 215 220				672
taa aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc tac Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr 225 230 235 240				720
att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg cca Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro 245 250 255				768
gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met 260 265 270				816
aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg gtc Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val 275 280 285				864
ttt gtg gga gcc tat acc ttc tgaagaccct cagggaggg ccatgtgggg Phe Val Gly Ala Tyr Thr Phe 290 295				915
gccccttcccc cctccccatag cttaaagcagc cccggggggcc tagggatgac cgttctgctt aaaggaacta tgatgtgaag gacaataaag ggagaaaagaa ggaaaa				975 1021

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<210> 9

<211> 295

<212> PRT

<213> Artificial sequence

<220>

<223> Murine MBP1 C-term fragment

<400> 9

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
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Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
180 185 190

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Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
275 280 285

Phe Val Gly Ala Tyr Thr Phe
290 295

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide c-myc 5'

<400> 10

gatccatgga gcagaagctg atctccgagg aggacctga 39

<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide c-myc 3'

<400> 11

gatctcaggc cttcctcgga gatcagcttc tgctccatg 39

<210> 12

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<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' MCS oligonucleotide

<400> 12
gatctcggtc gacctgcattt caattccggg gtgcggccgc gagct

45

<210> 13
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' MCS oligonucleotide

<400> 13
cgcggccgca cccgggaattt gcatgcaggc cgaccga

37

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide 3' mMBP1

<400> 14
cggtaactggc agaggtaact gg

22

<210> 15
<211> 1513
<212> DNA
<213> Artificial Sequence
<220>
<223> MBP1 murine (complete sequence)
<220>
<221> CDS
<222> (49)...(1377)

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Met Leu Pro		
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ttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg ttt ctg ctg	105	
Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu		
5 10 15		
ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc	153	
Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser		
20 25 30 35		
tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac	201	
Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His		
40 45 50		
tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt	249	
Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly		
55 60 65		
gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc	297	
Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys Leu Pro Arg		
70 75 80		
tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca	345	
Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro		
85 90 95		
gcg gcc cat gct caa caa cca aac cct tgc ccg cag ggc tac gag cct	393	
Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro		
100 105 110 115		
gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg	441	
Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu		
120 125 130		
cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac	489	
His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr		
135 140 145		
cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg	537	
Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val		
150 155 160		
gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac	585	
Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn		
165 170 175		
ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga	633	
Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly		
180 185 190 195		
cct aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc	681	
Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala		
200 205 210		
cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc	729	
Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg		
215 220 225		

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tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp 230 235 240	777
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val 245 250 255	825
aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu 260 265 270 275	873
ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala 280 285 290	921
cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr 295 300 305	969
cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser 310 315 320	1017
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln 325 330 335	1065
cct tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser 340 345 350 355	1113
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly 360 365 370	1161
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe 375 380 385	1209
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg 390 395 400	1257
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr 405 410 415	1305
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr 420 425 430 435	1353
gtc ttt gtg gga gcc tat acc ttc tgaagaccct cagggaggg ccatgtgggg Val Phe Val Gly Ala Tyr Thr Phe 440	1407
gccccttcccc cctccccatag cttaagcagc cccggggggcc tagggatgac cgttctgctt aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa	1467
	1513

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<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<400> 16

Met Leu Pro Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala
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Phe Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly
100 105 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
195 200 205

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Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
210 215 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
275 280 285

Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val
305 310 315 320

Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
435 440

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' hMBP1

<400> 17

ctccgctccg aggtgatgg c

21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide 5' hMBP1

<400> 18

tgttagctact ccagctacct c

21

<210> 19

<211> 1122

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

<400> 19

aagccagccg agccgccaga gccgcgggccc gcgggggtgt cgcgggccc accccaggat 60

gctccctgc gcctcctgccc tacccgggtc tctactgctc tggcgctgc tactgttgct 120

cttggatca gcttctccctc aggattctga agagcccgac agctacacgg aatgcacaga 180

tggctatgag tgggacccag acagccagca ctgccggat gtcaacgagt gtctgaccat 240

ccctgaggcc tgcaaggggg aatgaagtg catcaaccac tacggggct acttgtgcct 300

gccccgctcc gctgccgtca tcaacgacct acacggcgag ggaccccccgc caccagtgcc 360

tcccgctcaa caccccaacc cctgccaccaggatgag cccgacgatc aggacagctg 420

tgtggatgtg gacgagtgtg cccaggccct gcacgactgt cgccccagcc aggactgcc 480

taacttgccct ggctcctatc agtgcacctg ccctgatggc taccgcaaga tcgggcccga 540

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tggctcccttc cgctgccagt gcgagccggg	cttccagctg gggcctaaca	accgctccctg	660
tgttgatgtg aacgagtggt	acatgggggc cccatgcgag	cagcgctgct tcaactccta	720
tgggaccttc ctgtgtcgct	gccaccaggg ctatgagctg	catcggatg gcttctccctg	780
cagtatatt gatgagtgta	gctactccag ctacccctgt	cagtaccgct gcgtcaacga	840
gccaggccgt ttctccctgcc	actgcccaca gggttaccag	ctgctggcca cacgcctctg	900
ccaagacatt gatgagtgta	agtctggtgc gcaccagtgc	tccgaggccc aaacctgtgt	960
caacttccat gggggctacc	gctgcgtgga caccaaccgc	tgcgtggagc cctacatcca	1020
ggtctctgag aaccgctgtc	tctgcccggc ctccaaccct	ctatgtcgag agcagccttc	1080
atccattgtg caccgctaca	tgaccatcac ctcggagcgg	ag	1122

<210> 20
<211> 684
<212> DNA
<213> Artificial Sequence
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<223> Human MBP1 cDNA (partial sequence)

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tgtgagtcgt	gtgcgcacca	gtgctccgag	gccccaaacctt	gtgtcaactt	ccatgggggc	180
taccgctgctg	tggacaccaa	ccgctgcgtg	gagccctaca	tccaggtctc	tgagaaccgc	240
tgtctctgcc	cggcctccaa	ccctctatgt	cgagagcagc	tttcatccat	tgtgcaccgc	300
tacatgacca	tcacctcgga	gcggagcgtg	ccgcgtacg	tgttccagat	ccaggcgacc	360
tccgtctacc	ccgggtgccta	aatgccttt	cagatccgtg	ctggaaactc	gcagggggac	420
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cggggccagct	ctgtactgag	gctcaccgtc	ttttagggg	cctacacctt	ctgaggagca	600
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gagaaaggca	ataaaggag	aaag				684

<210> 21
<211> 1480

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<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<220>

<221> CDS

<222> (59)..(1387)

<400> 21

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Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala
1 5 10 15

ctg cta ctg ttg ctc ttg gga tca gct tct cct cag gat tct gaa gag 154
Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu
20 25 30

ccc gac agc tac acg gaa tgc aca gat ggc tat gag tgg gac cca gac 202
Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp
35 40 45

agc cag cac tgc cgg gat gtc aac gag tgt ctg acc atc cct gag gcc 250
Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
50 55 60

tgc aag ggg gaa atg aag tgc atc aac cac tac ggg ggc tac ttg tgc 298
Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65 70 75 80

ctg ccc cgc tcc gct gcc gtc atc aac gac cta cac ggc gag gga ccc 346
Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro
85 90 95

ccg cca cca gtg cct ccc gct caa cac ccc aac ccc tgc cca cca ggc 394
Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly
100 105 110

tat gag ccc gac gat cag gac agc tgt gtg gat gtg gac gag tgt gcc 442
Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala
115 120 125

cag gcc ctg cac gac tgt cgc ccc agc cag gac tgc cat aac ttg cct 490
Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
130 135 140

ggc tcc tat cag tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc 538
Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145 150 155 160

gag tgt gtg gac ata gac gag tgc cgc tac cgc tac tgc cag cac cgc 586
Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
165 170 175

tgc gtg aac ctg cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc 634
Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
180 185 190

cag ctg ggg cct aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac 682

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Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp		
195						200						205					
atg	ggg	gcc	cca	tgc	gag	cag	cgc	tgc	tgc	ttc	aat	tcc	tat	ggg	acc	ttc	730
Met	Gly	Ala	Pro	Cys	Glu	Gln	Arg	Cys	Phe	Asn	Ser	Tyr	Gly	Thr	Phe		
210						215					220						
ctg	tgt	cgc	tgc	cac	cag	ggc	tat	gag	ctg	cat	cg	gat	ggc	ttc	tcc		778
Leu	Cys	Arg	Cys	His	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser		
225						230				235						240	
tgc	agt	gat	att	gat	gag	tgt	agc	tac	tcc	agc	tac	ctc	tgt	cag	tac		826
Cys	Ser	Asp	Ile	Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr		
245						250					255						
cgc	tgc	gtc	aac	gag	cca	ggc	cgt	ttc	tcc	tgc	cac	tgc	cca	cag	ggt		874
Arg	Cys	Val	Asn	Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly		
260						265					270						
tac	cag	ctg	ctg	gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag		922
Tyr	Gln	Leu	Leu	Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu		
275						280					285						
tct	ggt	gct	cac	cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat		970
Ser	Gly	Ala	His	Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His		
290						295					300						
ggg	ggc	tac	cgc	tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc		1018
Gly	Gly	Tyr	Arg	Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile		
305						310					315					320	
cag	gtc	tct	gag	aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt		1066
Gln	Val	Ser	Glu	Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys		
325						330					335						
cga	gag	cag	cct	tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg		1114
Arg	Glu	Gln	Pro	Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser		
340						345					350						
gag	cgg	agc	gtg	ccc	gct	gac	gtg	ttc	cag	atc	cag	gct	acc	tcc	gtc		1162
Glu	Arg	Ser	Val	Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val		
355						360					365						
tac	ccc	ggt	gcc	tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag		1210
Tyr	Pro	Gly	Ala	Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln		
370						375					380						
ggg	gac	ttt	tac	att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc		1258
Gly	Asp	Phe	Tyr	Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val		
385						390					395					400	
ctc	gcc	cg	ccg	gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag		1306
Leu	Ala	Arg	Pro	Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu		
405						410					415						
atg	gtc	acc	atg	aat	tcc	ctc	atg	agc	tac	cg	gcc	agc	tct	gta	ctg		1354
Met	Val	Thr	Met	Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu		
420						425					430						
agg	ctc	acc	gtc	ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag	gagggagcca				1407	
Arg	Leu	Thr	Val	Phe	Val	Gly	Ala	Tyr	Thr	Phe							
435						440											

Conseiller.ST25
ccctccctgc agctacccta gctgaggagc ctgttgtgag gggcagaatg agaaaggcaa 1467
taaaggaga aag 1480

<210> 22
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Human MBP1 (complete sequence)
<400> 22
Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala
1 5 10 15

Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro
85 90 95

Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly
100 105 110

Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
165 170 175

Conseiller_ST25

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
210 215 220

Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
275 280 285

Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile
305 310 315 320

Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
420 425 430

Conseiller.ST25

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
435 440

<210> 23

<211> 817

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 cDNA (partial sequence)

<400> 23
gctgtggcag aaacccctga cttctgccc ccacccca gcctcaggat gctcccttt 60
gcctccgtcc tccccgggtc tttgctgctc tgggcgttc tgctgttgct cttgggagca 120
gcgtccccac aggatcccga ggagccggac agctacacgg aatgcacaga tggctatgag 180
tggatgcag acagccagca ctgcccggat gtcaacgagt gcctgaccat cccggaggct 240
tgcaagggtg agatgaaatg catcaaccac tacgggggtt atttgtgtct gcctcgctct 300
gctgccgtca tcagtgatct ccatggtgaa ggacctccac cgccagcggc ccatgctcaa 360
caaccaaacc cttgcccgcga gggctacgag cctgatgaac aggagagctg tgtggatgtg 420
gacgagtgtt cccaggcttt gcatgactgt cgccctagtc aggactgcca taacccct 480
ggctccctacc agtgcacctg ccctgatggt taccaaaaa ttggacccga atgtgtggac 540
atagatgagt gtcgttaccg ctattgccag catcgatgtg tgaacctgcc gggcttttt 600
cgatgccagt gtgagccagg cttccagttg ggacctaaca accgctttg tgtggatgtg 660
aatgagtgtg acatgggagc cccatgtgag cagcgctgt tcaactccta tgggaccc 720
ctgtgtcgct gtaaccaggg ctatgagctg caccggatg gcttccctg cagcgatatc 780
gatgagtgcg gctactccag ttacctctgc cagtacc 817

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-GAPDH oligonucleotide

<400> 24

cggagtcAAC ggatttggTC gtat

24

Conseiller.ST25

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-GAPDH oligonucleotide

<400> 25

agccttctcc atgggtgtga agac

24

<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-beta-actin oligonucleotide

<400> 26

cggttggcct tggggttcag ggggg

25

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-MBP1 oligonucleotide

<400> 27

gccctgatgg ttaccgcaag a

21

<210> 28

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense MBP1 oligonucleotide

Conseiller.ST25

<400> 28		
agccccatg gaagttgaca c	21	
<210> 29		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> sense-beta-actin oligonucleotide		
<400> 29		
gtggggcgcc ccaggcacca	20	
<210> 30		
<211> 1358		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Human MBP1 C-term fragment		
<220>		
<221> CDS		
<222> (1)..(885)		
<400> 30		
tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc gag tgt gtg gac	48	
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp		
1 5 10 15		
ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtg aac ctg	96	
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu		
20 25 30		
cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc cag ctg ggg cct	144	
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro		
35 40 45		
aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac atg ggg gcc cca	192	
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro		
50 55 60		
tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgc	240	
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys		
65 70 75 80		
cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc tgc agt gat att	288	
His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile		
85 90 95		
gat gag tgt agc tac tcc agc tac ctc tgt cag tac cgc tgc gtc aac	336	

Conseiller.ST25

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn	
100 105 110	
gag cca ggc cgt ttc tcc tgc cac tgc cca cag ggt tac cag ctg ctg	384
Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu	
115 120 125	
gcc aca cgc ctc tgc caa gac att gat gag tgt gag tct ggt gcg cac	432
Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His	
130 135 140	
cag tgc tcc gag gcc caa acc tgc aac ttc cat ggg ggc tac cgc	480
Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg	
145 150 155 160	
tgc gtg gac acc aac cgc tgc gtg gag ccc tac atc cag gtc tct gag	528
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu	
165 170 175	
aac cgc tgt ctc tgc ccg gcc tcc aac cct cta tgt cga gag cag cct	576
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro	
180 185 190	
tca tcc att gtg cac cgc tac atg acc atc acc tcg gag cgg agc gtg	624
Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val	
195 200 205	
ccc gct gac gtg ttc cag atc cag gcg acc tcc gtc tac ccc ggt gcc	672
Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala	
210 215 220	
tac aat gcc ttt cag atc cgt gct gga aac tcg cag ggg gac ttt tac	720
Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr	
225 230 235 240	
att agg caa atc aac aac gtc agc gcc atg ctg gtc ctc gcc cgg ccg	768
Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro	
245 250 255	
gtg acg ggc ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg	816
Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met	
260 265 270	
aat tcc ctc atg agc tac cgg gcc agc tct gta ctg agg ctc acc gtc	864
Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val	
275 280 285	
ttt gta ggg gcc tac acc ttc tgaggagcag gagggagcca ccctccctgc	915
Phe Val Gly Ala Tyr Thr Phe	
290 295	
agctacccta gctgaggagc ctgttgtgag gggcagaatg agaaaggcaa taaaggaga	975
aagaaagtcc tggggctga ggtggcggg tcacactgca ggaagcctca ggctgggca	1035
gggtggcact tggggggca ggccaagttc acctaaatgg gggctcttat atgttcaggc	1095
ccagggcccc ccattgacag gagctggag ctctgcacca cgagttcag tcaccccgag	1155
aggagaggag gtaacgagga gggcggactc caggccccgg cccagagatt tggacttggc	1215
tggcttgcag gggtcctaag aaactccact ctggacagcg ccaggaggcc ctgggttcca	1275

Conseiller.ST25
ttccttaactc tgcccaaact tgtacatttg gataagccct agtagttccc tgggcctgtt 1335
tttctataaa acgaggcaac tgg 1358

<210> 31
<211> 295
<212> PRT
<213> Artificial Sequence
<220>
<223> Human MBP1 C-term fragment

<400> 31

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu
165 170 175

Conseiller, ST25
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
180 185 190

Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
275 280 285

Phe Val Gly Ala Tyr Thr Phe
290 295

<210> 32

<211> 1663

<212> DNA

<213> Artificial Sequence

<220>
<223> murine fibulin 2 c-term fragment

<220>

<221> CDS

<222> (1)..(999)

<400> 32
gag ggc tct gaa tgt gtg gat gtg aat gag tgc gag aca ggt gtg cat 48
Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His
1 5 10 15

cgc tgt ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc 96
Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg
20 25 30

tgt gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc 144
Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys
35 40 45

att gat gtg aac gaa tgc tgg gtc tcg ccg ggc cgc ctg tgc cag cac 192
Page 23

Conseiller, ST25

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His	50	55	60	
aca tgt gag aac aca ccg ggc tcc tac cgc tgc tcc tgc gct gct ggc	65	70	75	240
Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly				
ttc ctt ttg gcc gca gat ggc aaa cat tgt gaa gat gtc aac gag tgc	85	90	95	288
Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys				
gag act cgg cgc tgc agc cag gaa tgt gcc aac atc tat ggc tcc tat	100	105	110	336
Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr				
cag tgc tac tgc cgt cag ggc tac cag ctg gca gag gat ggg cat acc	115	120	125	384
Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr				
tgc aca gac atc gat gag tgt gca cag ggc gcg ggc att ctc tgt acc	130	135	140	432
Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr				
ttc cgc tgt gtc aac gtg cct ggg agc tac cag tgt gca tgc cca gag	145	150	155	480
Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu				
caa ggg tat aca atg atg gcc aac ggg agg tcc tgc aag gac ctg gat	165	170	175	528
Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp				
gag tgt gca ctg ggc acc cac aac tgc tct gag gct gag acc tgc cac	180	185	190	576
Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His				
aat atc cag ggg agt ttc cgc tgc ctg cgc ttt gat tgt cca ccc aac	195	200	205	624
Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn				
tat gtc cgt gtc tca caa acg aag tgc gag cgc acc aca tgc cag gat	210	215	220	672
Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp				
atc acg gaa tgt caa acc tca cca gct cgc atc acg cac tac cag ctc	225	230	235	720
Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu				
aat ttc cag aca ggc cta ctg gta cct gca cat atc ttc cgc atc ggc	245	250	255	768
Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly				
cct gct ccc gcc ttt gct ggg gac acc atc tcc ctg acc atc acg aag	260	265	270	816
Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys				
ggc aat gag gag ggc tac ttc gtc aca cgc aga ctc aat gcc tac act	275	280	285	864
Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr				
ggt gtg gta tcc ctg cag cgg tct gtt ctg gag ccg cgg gac ttt gcc	290	295	300	912
Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala				

Conseiller.ST25

cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc	960
Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe	
305 310 315 320	
ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgaggtgaca	1009
Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro	
325 330	
tgtcaggcaa tcccctcagg tcatgcctgg gcgggtggca gctgcgccac tcctaagtgg	1069
cttttgctg tgactctgta acttaactta atcatgctga gctgggttgt cttgagtctc	1129
tacccttagag ggagggagat gcaccccagc aggcaactgag tacaggccag ggtcacccga	1189
ggctagatgg tgacctgcaa actggaaaca gccatagggg gcttctgaac tccactcctc	1249
aactatggct acagctgaca ttccattcct tcattccactg tgttcctcaa ttaaaaaaaaa	1309
aaatcagctg tgcattgttag cacagacctt taatcctagc actggggagg cagaggtagg	1369
tagatctctg agttccaggc cagcctggtc tacactggga gttctaacca gccagagcta	1429
catagagaga ccctatctca acaaggaaaa aacgaaagaa atctctgtga gttccaggcc	1489
agcctggtct acgctgggag ttcttaaccag ccagagctac atagagagat cctatctcaa	1549
caaggaaaaa tggaaagaaat cattttaaaa ggttttttt tttgctgttg ttgtttaatg	1609
ataagagtag cacatataca ttattaaaaa tgatcaaata gcacagaaag gtta	1663

<210> 33

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine fibulin 2 c-term fragment

<400> 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His
1 5 10 15

Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg
20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys
35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His
50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly
65 70 75 80

Conseiller.ST25

Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys
85 90 95

Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr
100 105 110

Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr
115 120 125

Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr
130 135 140

Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu
145 150 155 160

Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp
165 170 175

Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His
180 185 190

Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn
195 200 205

Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp
210 215 220

Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu
225 230 235 240

Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly
245 250 255

Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys
260 265 270

Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr
275 280 285

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala
290 295 300

Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe
305 310 315 320

Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro
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325

Conseiller.ST25
330

<210> 34

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine N-terminal signal sequence

<400> 34

Ala Val Ala Glu Thr Pro Asp Phe Cys Pro Pro Pro Pro Ser Leu Arg
1 5 10 15

<210> 35

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Human N-terminal signal sequence

<400> 35

Ser Gln Pro Ser Arg Gln Ser Arg Gly Pro Arg Gly Cys Arg Gly Pro
1 5 10 15

Asn Pro Arg